

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 25, 2002, 05:58:15 ; Search time 2251.99 Seconds
(without alignments)
12849.734 Million cell updates/sec

Title: US-09-821-839-1
Perfect score: 2144
Sequence: 1 actgataagccactctct.....aaaaaaaaaaaaaaaa 2144

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: em_estb:*

- 2: em_estb:*
- 3: em_estb:*
- 4: em_estb:*
- 5: em_estb:*
- 6: em_estb:*
- 7: em_estb:*
- 8: em_estb:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609.8	28.4	1233	12	B10183
2	188.8	8.8	192	12	B97951
3	188.8	8.8	818	12	BH530370
4	175	8.2	531	10	BF291837
5	172.6	8.1	1166	12	B12531
6	165.2	7.7	803	12	BH530380
7	152.4	7.1	465	12	BH462012
8	147.4	6.9	727	12	BH487741
9	116.8	5.4	336	12	CNS008M
10	96.4	4.5	498	10	BM270448
11	93.2	4.3	612	12	BH477964
12	80.8	3.8	605	12	BH462017
13	70.6	3.3	791	12	AZ686821
14	70.4	3.3	668	9	AL514901
15	68.8	3.2	1225	12	CNS0161D
16	68.4	3.2	1309	10	BE420736
17	68	3.2	1101	12	CNS001FB

18	67.8	3.2	330	9	AL513817
19	67.8	3.2	634	9	AL514047
20	67.6	3.2	410	9	AL513713
21	67.6	3.2	590	9	AL515321
22	67.4	3.1	423	9	AM119922
23	67.2	3.1	613	12	A0922590
24	67	3.1	661	12	CNS04QDH
25	66.2	3.1	987	12	CNS014PQ
26	65.8	3.1	388	12	CNS039K1
27	65.8	3.1	401	9	AL515191
28	65.6	3.1	329	9	AL513719
29	65.6	3.1	456	9	AL513813
30	65.6	3.1	523	9	AL514015
31	65.6	3.1	619	9	AL514935
32	65.4	3.1	329	9	AL513719
33	65.4	3.1	421	10	BM270739
34	65.2	3.0	714	12	A0324694
35	65.2	3.0	777	12	CNS025MB
36	65.2	3.0	988	12	CNS0072R
37	65	3.0	250	10	BF742555
38	64.6	3.0	230	9	AL511812
39	64.2	3.0	453	10	BF298095
40	64.2	3.0	767	10	BE874847
41	64.2	3.0	618	12	AL055924
42	64.2	3.0	951	12	AZ672893
43	64	3.0	954	12	BH162327
44	63.8	3.0	279	9	AL540752
45	63.8	3.0	633	9	AL513979

ALIGNMENTS

RESULT 1
LOCUS B10183/c
DEFINITION F19N12-SP6 IGF Arabidopsis thaliana genomic clone F19N12, DNA sequence.
ACCESSION B10183
VERSION B10183.1 GI:2091302
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.
REFERENCE 1 (bases 1 to 1233)
Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.
AUTHORS
TITLE BAC End Sequences at ATCC
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: F19N12-77
Contact: Ecker J.
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Seq primer: Sp6
Class: BAC ends
High quality sequence start: 87
High quality sequence stop: 806.
Location/Qualifiers
1..1233
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="F19N12"
/clone_1db="IGF"
/sex="hermaphrodite"
/note="Vector: pBelbacII; Site_1: EcoRI; Site_2: EcoRI;

